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RAW SEQUENCE LISTING

DATE: 06/10/2004

PATENT APPLICATION: US/10/632,929

TIME: 20:11:44

Input Set : N:\CrF3\RULE60\10632929.txt

Output Set: N:\CRF4\06102004\J632929.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: WALLACH, David

6 BIGDA, Jacek

7 BELETSKY, Igor

8 METT, Igor

10 (ii) TITLE OF INVENTION: TNF LIGANDS

12 (iii) NUMBER OF SEQUENCES: 17

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: BROWDY AND NEIMARK

16 (B) STREET: 419 Seventh Street, N.W.

17 (C) CITY: Washington

18 (D) STATE: D.C.

19 (E) COUNTRY: USA

20 (F) ZIP: 20004

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/632,929

C--> 30 (B) FILING DATE: 04-Aug-2003

31 (C) CLASSIFICATION:

40 (vii) PRIOR APPLICATION DATA:

W--> 34 (A) APPLICATION NUMBER: US/08/115,685

35 (B) FILING DATE: 03-SEP-1993

W--> 37 (A) APPLICATION NUMBER: IL 103051

38 (B) FILING DATE: 03-SEP-1992

W--> 41 (A) APPLICATION NUMBER: IL 106271

42 (B) FILING DATE: 08-JUL-1993

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Townsend, G. Kevin

46 (B) REGISTRATION NUMBER: 34,033

47 (C) REFERENCE/DOCKET NUMBER: WALLACH=10

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 202-628-5197

51 (B) TELEFAX: 202-737-3528

52 (C) TELEX: 248633

55 (2) INFORMATION FOR SEQ ID NO: 1:

57 (i) SEQUENCE CHARACTERISTICS:

58 (A) LENGTH: 58 amino acids

59 (B) TYPE: amino acid

ENTERED

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60      (C) STRANDEDNESS: single
61      (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: peptide
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70      Ala Gln Val Phe Thr Thr His Gln Ile Cys Asn Val Val Ala Ile Pro
71      1      5      10      15
73      Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Val
74      20      25      30
76      Asp Phe Ala Leu Pro Val Gly Leu Ile Cys Asn Val Val Ala Ile Pro
77      35      40      45
79      Gly Asn Ala Ser Met Asp Ala Val Cys Thr
80      50      55
82 (2) INFORMATION FOR SEQ ID NO: 2:
83      (i) SEQUENCE CHARACTERISTICS:
84      (A) LENGTH: 2224 base pairs
85      (B) TYPE: nucleic acid
86      (C) STRANDEDNESS: single
87      (D) TOPOLOGY: linear
88      (ii) MOLECULE TYPE: cDNA
89      (ix) FEATURE:
90      (A) NAME/KEY: CDS
91      (B) LOCATION: 90..1472
92      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
100 GCGAGCGCAG CGGAGCCTGG AGAGAAGGCG CTGGGCTGCG AGGGCGCGAG GGCGCGAGGG      60
102 CAGGGGGCAA CCGGACCCCG CCCGCACCC ATG GCG CCC GTC GCC GTC TGG GCC      113
103      Met Ala Pro Val Ala Val Trp Ala
104      1      5
106 GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC      161
107 Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro
108      10      15      20
110 GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC      209
111 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
112      25      30      35      40
114 CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA      257
115 Arg Leu Arg Glu Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
116      45      50      55
118 TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC      305
119 Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp
120      60      65      70
122 ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC      353
123 Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn
124      75      80      85
126 TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG      401
127 Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln
128      90      95      100
130 GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC      449
131 Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
132      105      110      115      120
134 AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG      497

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135	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	
136					125					130					135		
138	TGC	GCG	CCG	CTG	CGC	AAG	TGC	CGC	CCG	GGC	TTC	GGC	GTG	GCC	AGA	CCA	545
139	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	
140				140						145					150		
142	GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC	CCG	GGG	ACG	593
143	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
144			155					160					165				
146	TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	641
147	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
148		170					175					180					
150	TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	689
151	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
152	185					190				195					200		
154	ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	737
155	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
156				205					210					215			
158	CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	785
159	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
160				220					225					230			
162	CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	833
163	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
164			235				240						245				
166	CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	881
167	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
168		250				255					260						
170	ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	929
171	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
172	265				270				275						280		
174	TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	977
175	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
176				285					290					295			
178	GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	1025
179	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
180			300						305					310			
182	GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	1073
183	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
184			315				320						325				
186	AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	1121
187	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	
188		330				335					340						
190	CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	1169
191	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
192	345				350				355						360		
194	GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	1217
195	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	
196			365						370					375			
198	ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	1265
199	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	

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200          380          385          390
202 CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG GGA GAC ACA      1313
203 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr
204          395          400          405
206 GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG GTC CCC TTC TCC      1361
207 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser
208          410          415          420
210 AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG ACG CCA GAG ACC CTG      1409
211 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu
212 425          430          435          440
214 CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT      1457
215 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala
216          445          450          455
218 GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC      1512
219 Gly Met Lys Pro Ser
220          460
222 TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG      1572
224 GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT      1632
226 CTGACCTGCA GGCCAAGAGC AGAGGCAGCG AGTTGGGGAA AGCCTCTGCT GCCATGGTGT      1692
228 GTCCCTCTCG GAAGGCTGGC TGGGCATGGA CGTTCGGGGC ATGCTGGGGC AAGTCCCTGA      1752
230 CTCTCTGTGA CCTGCCCCGC CCAGCTGCAC CTGCCAGCCT GGCTTCTGGA GCCCTTGGGT      1812
232 TTTTGTGTTG TTTGTTTGTG TGTTTGTGTT TTTCTCCCCC TGGGCTCTGC CCAGCTCTGG      1872
234 CTTCCAGAAA ACCCCAGCAT CCTTTTCTGC AGAGGGGCTT TCTGGAGAGG AGGGATGCTG      1932
236 CCTGAGTCAC CCATGAAGAC AGGACAGTGC TTCAGCCTGA GGCTGAGACT GCGGGATGGT      1992
238 CCTGGGGCTC TGTGTAGGGA GGAGGTGGCA GCCCTGTAGG GAACGGGGTC CTTCAAGTTA      2052
240 GCTCAGGAGG CTTGGAAAGC ATCACCTCAG GCCAGGTGCA GTGGCTCACG CCTATGATCC      2112
242 CAGCACTTTG GGAGGCTGAG GCGGGTGGAT CACCTGAGGT TAGGAGTTCG AGACCAGCCT      2172
244 GGCCAACATG GTAAACCCCC ATCTCTACTA AAAATACAGA AATTAGCCCG GC      2224
247 (2) INFORMATION FOR SEQ ID NO: 3:
249 (i) SEQUENCE CHARACTERISTICS:
250 (A) LENGTH: 461 amino acids
251 (B) TYPE: amino acid
252 (D) TOPOLOGY: linear
254 (ii) MOLECULE TYPE: protein
256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
258 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
259 1          5          10          15
261 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
262          20          25          30
264 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
265          35          40          45
267 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
268          50          55          60
270 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
271 65          70          75          80
273 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
274          85          90          95
276 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
277          100          105          110

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```

279 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
280      115      120      125
282 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
283      130      135      140
285 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
286      145      150      155      160
288 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
289      165      170      175
291 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
292      180      185      190
294 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
295      195      200      205
297 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
298      210      215      220
300 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
301      225      230      235      240
303 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
304      245      250      255
306 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
307      260      265      270
309 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
310      275      280      285
312 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
313      290      295      300
315 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
316      305      310      315      320
318 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
319      325      330      335
321 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
322      340      345      350
324 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
325      355      360      365
327 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
328      370      375      380
330 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
331      385      390      395      400
333 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
334      405      410      415
336 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
337      420      425      430
340 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
341      435      440      445
343 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
344      450      455      460

```

346 (2) INFORMATION FOR SEQ ID NO: 4:

348 (i) SEQUENCE CHARACTERISTICS:

349 (A) LENGTH: 345 base pairs

350 (B) TYPE: nucleic acid

351 (C) STRANDEDNESS: single